the complex comprising less than the CD163 receptor binding region are also comprised in the present invention. Functionally equivalent complex peptides, and fragments thereof according to the present invention, may comprise less or more amino acid residues than CD163 receptor binding region.

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Fragments comprising the CD163 receptor binding region of HP-Hb complex preferably comprises regions capable of binding to the SRCR domains I-IX of the CD163 receptor, such as capable of binding to a region in the SRCR domains I-VII of the CD163 receptor, capable of binding to a region in the SRCR domains I-VII of the CD163 receptor, capable of binding to a region in the SRCR domains I-VI of the CD163 receptor, capable of binding to a region in the SRCR domains I-V of the CD163 receptor, capable of binding to a region in the SRCR domains I-IV of the CD163 receptor, capable of binding to a region in the SRCR domains I-III of the CD163 receptor, capable of binding to a region in the SRCR domains I-III of the CD163 receptor, capable of binding to a region in the SRCR domains I-III of the CD163 receptor.

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Fragments of the complex preferably comprises at least the heavy chain (β) of haptoglobin or a part of said chain capable of forming complex with haemoglobin.

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In particular the fragments may comprise a sequence corresponding to an 103-347 of splP00737 in Fig. 4 or to an 162-406 of splP00738.

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In one embodiment mimics may be understood to exhibit amino acid sequences gradually differing from the preferred predetermined sequence, as the number and scope of insertions, deletions and substitutions including conservative substitutions increases. This difference is measured as a reduction in homology between the predetermined sequence and the mimic.

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All functional equivalents of Hp-Hb complexes are included within the scope of this invention, regardless of the degree of homology that they show to a predetermined sequence of Hp-Hb complexes. The reason for this is that some regions of the complex are most likely readily mutatable, or capable of being completely deleted, without any significant effect on the binding activity of the resulting fragment.

A functional equivalent obtained by substitution may well exhibit some form or degree of native Hp-Hb activity, and yet be less homologous, if residues containing functionally similar amino acid side chains are substituted. Functionally similar in this respect refers to dominant characteristics of the side chains such as hydrophobic, basic, neutral or acidic, or the presence or absence of steric bulk. Accordingly, in one embodiment of the invention, the degree of identity between i) a given complex equivalent capable of effect and ii) a preferred predetermined fragment, is not a principal measure of the fragment as a variant or functional

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equivalent of a preferred predetermined complex fragment according to the present invention.

Fragments sharing at least some homology with a preferred predetermined complex fragment of at least 50 amino acids, more preferably at least 100 amino acids, are to be considered as falling within the scope of the present invention when they are at least about 40 percent homologous with the preferred predetermined Hp-Hb complex or fragment thereof, such as at least about 50 percent homologous, for example at least about 60 percent homologous, such as at least about 70 percent homologous, for example at least about 75 percent homologous, such as at least about 80 percent homologous, for example at least about 85 percent homologous, such as at least about 90 percent homologous, for example at least 92 percent homologous, such as at least 94 percent homologous, for example at least 95 percent homologous, such as at least 95 percent homologous, such as at least 96 percent homologous, for example at least 97 percent homologous, such as at least 98 percent homologous, for example at least 99 percent homologous, such as at least 98 percent homologous, for example at least 99 percent homologous, such as at least 98 percent homologous, for example at least 99 percent homologous, such as at least 98 percent homologous, for example at least 99 percent homologous bomologous with the predetermined complex fragment. In a preferred embodiment the above percentages for homologous are leats to percentage identity.

The Hp-Hb complex is preferably constituted of at least two different chains (sequences) wherein one chain constitutes the haptoglobin part of the complex and the other chain constitutes the haemoglobin part. A mimic of the Hp-Hb complex may however be constituted by one chain (sequence) or multimers of said chain, wherein the chain is a steric equivalent of the Hp-Hb complex.

In addition to the mimics described herein, sterically similar variants may be formulated to mimic the key portions of the variant structure and that such compounds may also be used in the same manner as the variants of the invention. This may be achieved by techniques of modelling and chemical designing known to those of skill in the art. It will be understood that all such sterically similar constructs fall within the scope of the present invention.

In one embodiment the Hp-Hb complex or parts thereof or mimics thereof is synthesised by automated synthesis. Any of the commercially available solid-phase techniques may be employed, such as the Merrifield solid phase synthesis method, in which amino acids are sequentially added to a growing amino acid chain. Equipment for automated synthesis of polypeptides is commercially available from suppliers such as Applied Biosystems, Inc. of Foster City, Calif., and may generally be operated according to the manufacturer's instructions. Solid phase synthesis will enable the incorporation of desirable amino acid substitutions into any Hp-Hb complex according to the present invention. It will be understood that substitutions, deletions, insertions or any subcombination thereof may be combined to arrive at a final sequence of a functional equivalent. Insertions shall be understood to include amino-

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terminal and/or carboxyl-terminal fusions, e.g. with a hydrophobic or immunogenic protein or a carrier such as any polypeptide or scaffold structure capable as serving as a carrier.

Hp-Hb complexes according to the invention may be synthesised both in vitro and in vivo. Methods for in vitro synthesis are well known. When synthesized in vivo, a host cell is transformed with vectors containing DNA encoding various parts of the Hp-Hb complex. A vector is defined as a replicable nucleic acid construct. Vectors are used to mediate expression of the Hp-Hb complex. An expression vector is a replicable DNA construct in which a nucleic acid sequence encoding the predetermined Hp-Hb complex, or any functional equivalent thereof that can be expressed in vivo, is operably linked to suitable control sequences capable of effecting the expression of the variant, or equivalent in a suitable host. Such control sequences are well known in the art.

A DNA sequence encoding the various parts of the Hp-Hb complex is meaning a DNA sequence encoding the haptoglobin part and a DNA sequence encoding the haemoglobin part. In another embodiment the DNA sequence may be one sequence encoding one peptide sequence which post-translationally is cleaved into the haptoglobin part and the haemoglobin part. In yet another embodiment one peptide constituting both parts is not cleaved, but due to post-translationally folding and/or processing functions as the complex.

Accordingly, one aspect of the invention relates to a DNA sequence encoding a Hp-Hb complex as defined above, the DNA sequence may be a genomic DNA sequence, a cDNA sequence or a mixture of a genomic and a cDNA sequence.

Furthermore, the invention relates to a vector comprising the DNA sequence, as well as to a cell comprising said vector, said cell being capable of expressing the DNA sequence, either as a Hp-Hb complex released into the cell culturing media, or a Hp-Hb complex anchored to the cell membrane.

Cultures of cells may be derived from prokaryotic and eukaryotic cells. In principle, any higher eukaryotic cell culture is workable, whether from vertebrate or invertebrate culture but human cells are preferred. Examples of useful host cell lines E.coli, yeast, or human cell lines. Preferred host cells are eukaryotic cells known to synthesize endogenous haptoglobin and/or haemoglobin. Cultures of such host cells may be isolated and used as a source of the variant, or used in therapeutic methods of treatment, including therapeutic methods aimed at diagnostic methods carried out on the human or animal body.

In order to increase the binding affinity the Hp-Hb complex or part thereof or mimic thereof is preferably dimeric. In a more preferred embodiment the the Hp-Hb complex or a part thereof